## SCORE Search Results Details for Application 09426011 and Search Result 20070320\_085442\_us-09-426-011d-4.rag.

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GenCore version 6.2 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 20, 2007, 15:53:45; Search time 281 Seconds

(without alignments)

19.130 Million cell updates/sec

Title:

US-09-426-011D-4

Perfect score: 64

Sequence:

1 RRRPRPPYLPR 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters:

2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A Geneseq\_200701:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\* 4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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GenCore version 6.2 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 20, 2007, 15:53:45; Search time 205 Seconds (without alignments)

19.130 Million cell updates/sec

Title:

US-09-426-011D-5

Perfect score: 48

Sequence:

1 RRRPRPPY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters:

2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A\_Geneseq\_200701:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\* 4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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GenCore version 6.2 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 20, 2007, 15:55:10 ; Search time 269 Seconds

(without alignments)

43.902 Million cell updates/sec

Title: US-09-426-011D-4

Perfect score: 64

Sequence:

1 RRRPRPPYLPR 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

3281787 seqs, 1072124677 residues -

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

UniProt\_8.4:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Qúery Match	Length	DB	ID	Description
1	64	100.0	172	1	PR39_PIG	P80054 sus scrofa
2	51	79.7	194	2	Q6Z0W1_ORYSA	Q6z0w1 oryza sativ
· 3	50	78.1	1192	2	Q40W17_KINRA	Q40w17 kineococcus

# SCORE Search Results Details for Application 09426011 and Search Result 20070320\_085445\_us-09-426-011d-5.rup.

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GenCore version 6.2 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 20, 2007, 15:55:10; Search time 195 Seconds (without alignments)

43.902 Million cell updates/sec

Title: US-09-426-011D-5

List

Perfect score: 48

Sequence: 1 RRRPRPPY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt\_8.4:\*

1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.		Query Match	Length	DB	ID	Description
1	48	100.0			PR39_PIG	P80054 sus scrofa
2	43	89.6	142	2	Q6Z2A8_ORYSA	Q6z2a8 oryza sativ
3	43	89.6	344	2	Q2J6J4_FRASC	Q2j6j4 frankia sp.

## SCORE Search Results Details for Application 09426011 and Search Result 20070320\_085448\_us-09-426-011d-4.rpr.

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GenCore version 6.2 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 20, 2007, 16:04:42; Search time 29 Seconds (without alignments)

36.562 Million cell updates/sec

Title: US-09-426-011D-4

List

Perfect score: 64

Sequence: 1 RRRPRPPYLPR 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Pi

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result Query
No. Score Match Length DB ID Description

1 64 100.0 172 2 S68232 antimicrobial prot

## SCORE Search Results Details for Application 09426011 and Search Result 20070320 085451 us-09-426-011d-4.rai.

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GenCore version 6.2 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 20, 2007, 16:12:54; Search time 43 Seconds

(without alignments)

22.174 Million cell updates/sec

Title:

US-09-426-011D-4

Perfect score: 64

Sequence:

1 RRRPRPPYLPR 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters:

650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents AA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6\_COMB.pep:\* 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H\_COMB.pep:\* 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\* 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*

/EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result

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## SCORE Search Results Details for Application 09426011 and Search Result 20070320\_085451\_us-09-426-011d-5.rai.

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GenCore version 6.2 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 20, 2007, 16:12:54; Search time 32 Seconds (without alignments)

22.174 Million cell updates/sec

Title: US-09-426-011D-5

Perfect score: 48

Sequence: 1 RRRPRPPY 8

Scoring table: BLOSUM62

SLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result

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## SCORE Search Results Details for Application 09426011 and Search Result 20070320\_085454\_us-09-426-011d-4.rapbm.

Score Home Page **Retrieve Application** 

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SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 09426011 and Search Result 20070320\_085454\_us-09-426-011d-4.rapbm.

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GenCore version 6.2 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 20, 2007, 16:13:01; Search time 156 Seconds

(without alignments)

32.718 Million cell updates/sec

Title: US-09-426-011D-4

Perfect score: 64

Sequence: 1 RRRPRPPYLPR 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database : Published\_Applications\_AA\_Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result Query

No. Score Match Length DB ID

Description

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GenCore version 6.2 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 20, 2007, 16:13:01; Search time 113 Seconds

(without alignments)

32.718 Million cell updates/sec

Title:

US-09-426-011D-5

Perfect score: 48

Sequence: 1 RRRPRPPY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters:

2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database :

Published\_Applications\_AA\_Main:\*

1: /EMC Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:\*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\* 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Query

No. Score Match Length DB ID

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Description

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GenCore version 6.2 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 20, 2007, 16:14:56; Search time 67 Seconds (without alignments)

31.686 Million cell updates/sec

Title: US-09-426-011D-4

Perfect score:

Sequence: 1 RRRPRPPYLPR 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 848676 seqs, 191783220 residues

Total number of hits satisfying chosen parameters: 848676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

2: /EMC Celerra SIDS3/ptodata/1/pubpaa/US06 NEW\_PUB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

/EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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GenCore version 6.2 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 20, 2007, 16:14:56; Search time 48 Seconds (without alignments)

31.686 Million cell updates/sec

Title:

US-09-426-011D-5

Perfect score: 48

Sequence:

1 RRRPRPPY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

848676 seqs, 191783220 residues

Total number of hits satisfying chosen parameters:

848676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published\_Applications AA New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

3: /EMC Celerra SIDS3/ptodata/1/pubpaa/US07 NEW PUB.pep:\* 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\* 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

/EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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